Morphological Variation of Ten *Tilapia guineensis* Populations in Selected Rivers in Nigerian coastal waters

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Abstract

A morphological study was carried out on *Tilapia guineensis*, a fish species of considerable dietary importance commonly found in Nigerian coastal waters. Principal component analysis (PCA) revealed two principal components (PC-1 and PC-11) that accounted for 90.3% of observed variation in morphometric attributes; 58.1% and 58.8% in meristics and truss network system respectively. When compared to other locations, fish in Iwoama had the highest mean weight of 0.29 ± 0.006kg with a mean total length of 0.24 ± 0.002m ($p<0.05$). Truss network data showed that Brass location had the highest mean length of 0.149 ± 0.001m. Among the thirteen morphometric variables considered, pre-anal length (PAL) and standard length were the most correlated ($r = 0.96$; $p<0.01$) while dorsal fin count (DFC) and anal fin count (AFC) were the most correlated (0.37; $p<0.01$) among the meristic variables. Cluster analysis revealed three clusters for meristic variables and two clusters for morphometric and truss network variables respectively. These findings could be attributed to gene flow between widely distributed sub-populations of *T. guineensis*. However, this fish still possess sufficient variability for possible genetic improvement through breeding.

Keywords: Morphometrics; meristics; truss network; principal component analysis; *Tilapia guineensis*; Nigerian coastal waters.

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1.   Introduction

Tilapia guineensis is a typical estuarine cichlid species found in abundance in many lagoons and coastal brackish lakes [1]. Tilapia, a large genus in cichlid family – (Cichlidae), is the third largest fish taxon and one of the most diverse fish genera in the world [2]. *Tilapia guneensis*, one of the most important species in the genus Tilapia in Nigeria, and it has continued to contribute immensely to the nutritional needs, economic growth and development of many nations including Nigeria.

From previous studies, [3] reported that analysis of phenotypic variation in morphometric characters or meristic counts is the method most commonly used to delineate stocks of fish. These conventional techniques have been improved to give a modern landmark-based technique called Truss network system [4].

The Truss Network System covers the entire fish in a uniform network, and theoretically should increase the likelihood of extracting morphometric differences within and between species. Although much work has been done on the use of morphological methods to characterize many fish species, there is dearth of information on the use of these methods on *T. guineensis*. The widespread and mixing of two or more tilapia species in natural water bodies makes the identification of *Tilapia guineensis* to be difficult by mere traditional method. There is then need to address the taxonomic problems and also to identify the distinctness of both natural and aquaculture populations using truss network amongst the conventional methods. In this context, we have investigated the comparative significance of three morphological methods (morphometric, meristic and truss network system) in assessing morphological variations among ten *T. guineensis* populations in Nigerian coastal waters with a view to recommending the method that differentiates the fish well for future studies.

2.   Materials and Methods

A total of 500 samples of both male and female *Tilapia guineensis* fish weighing 20-357g were randomly collected from ten selected coastal rivers in five coastal states of Nigeria (Figure 1). Fifty fish samples from each location were obtained from the respective locations through the help of fishermen at the landing sites and were first frozen and transported to the Biotechnology Laboratory of Nigerian Institute for Oceanography and Marine Research, Lagos, in ice and were identified by a fish taxonomist from the Institute then stored at -20°C until used for detailed analyses. A total of 35 morphological characters were measured which included 13 morphometric variables, five meristic variables and 17 truss network characters which were directly counted and measured to the nearest 0.1 cm using a thread and measuring board.

Measurements of body parts were made with the head of fish pointing left. Since meristic characters were independent of size of the fish and did not change during growth [5] the raw meristic data were used in analysis. However, to avoid possible biases produced by size effects on the morphometric variables, all morphometric characters were standardized by dividing the measurement by the standard length of each fish to minimize the effect of fish size [6].
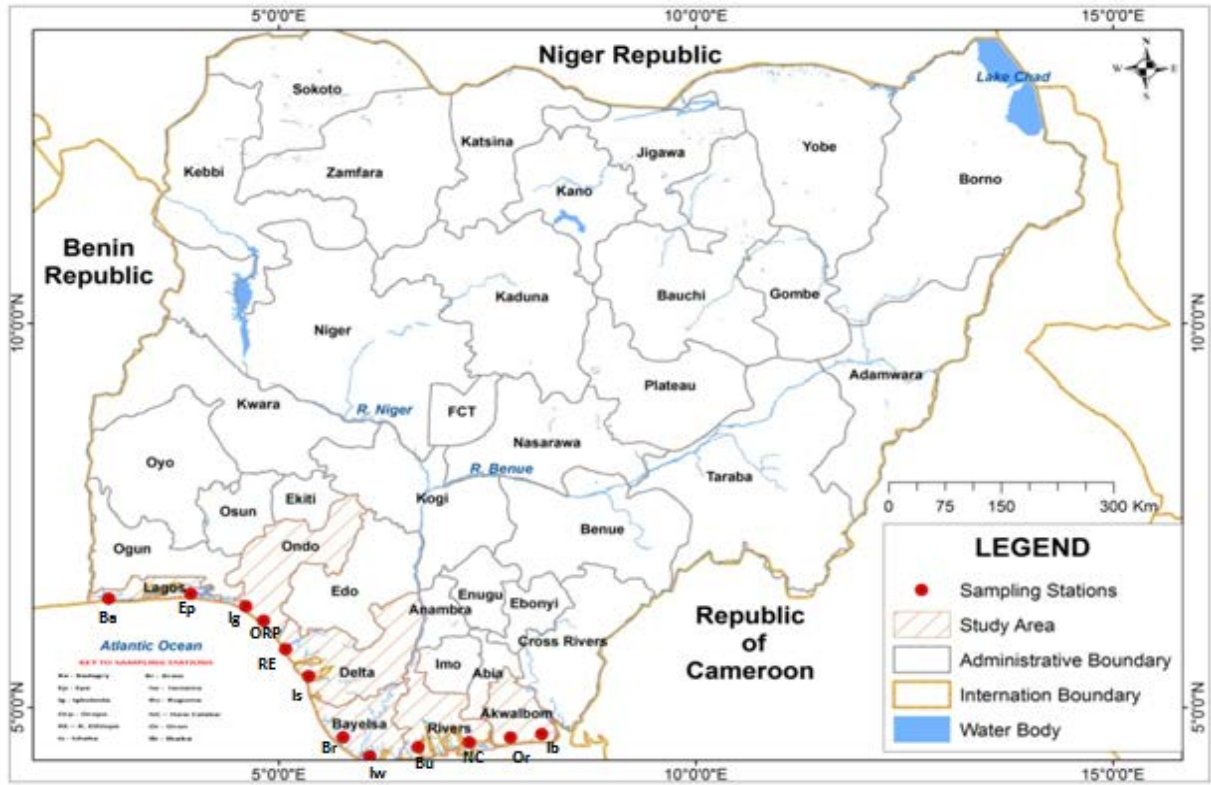
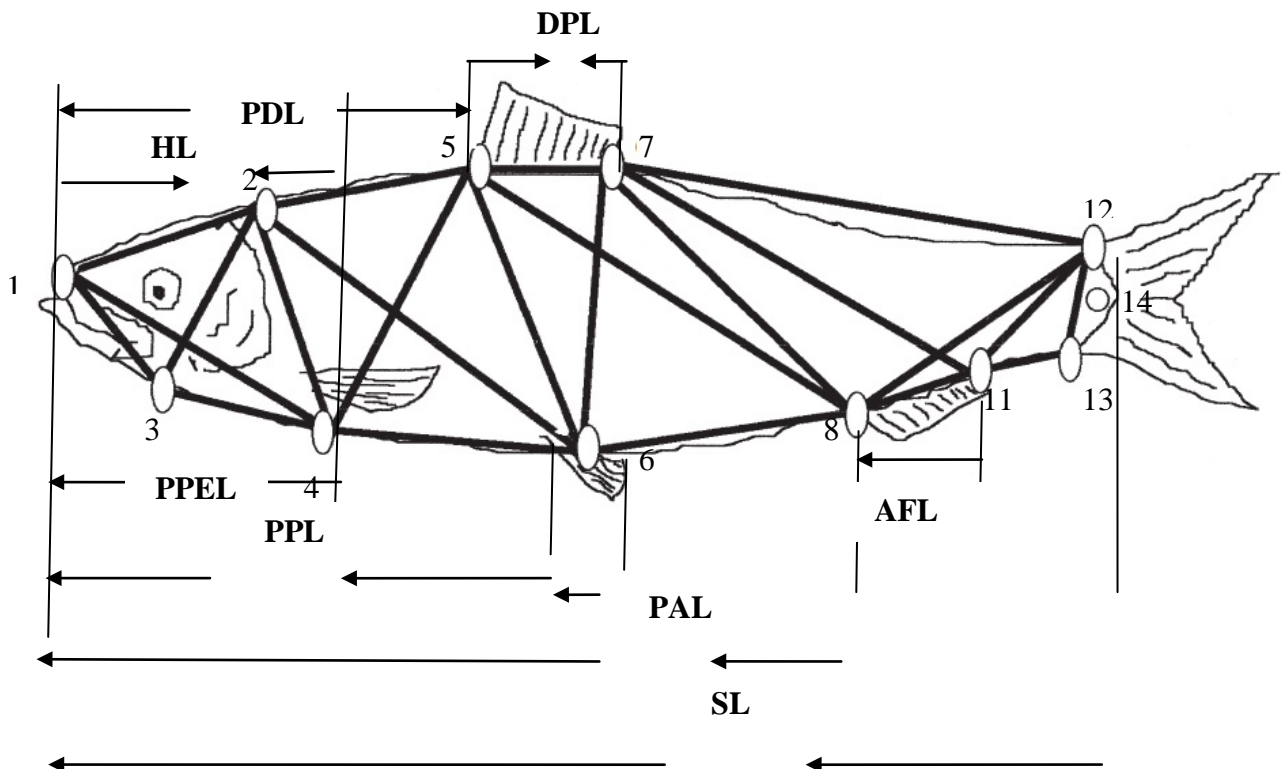**Figure 1:** Map of Nigeria Showing Sampling Stations.

Figure 2: Conventional Dimensions and Position of Truss network Measured for Morphological Variation

2.1   *Truss measurements*

The shape of each sample specimen was measured by truss network method according to Sathianandan, [7]. Figure 2 shows the landmark points in a truss network measurement. The landmarks were linked closely to the skeletal structure of tilapia, and were observed easily observed visually.

2.2   *Statistical Analysis*

Analysis was carried out separately for morphometric, meristic and truss characters using statistical tool for Agricultural Research (STAR) version 2.0. The body shape data were subjected to principal components analysis (PCA) in order to reduce the variables to principal component that can explain most of the variation observed in the data. Comparison of mean was by analysis of variance (ANOVA) followed by Duncan post-hoc analysis. Difference between means were considered significant when $p<0.05$.

3.   Results

3.1   *Morphometric Analysis*

Analysis of morphometric data showed that the first principal component (PC-I) accounted for 85.73% while the second (PC-II) accounted for 4.54% giving a total 90.27% of the variations in morphometric measurements data and were used to explain the variations. The highest mean weight and total length (0.29 ± 0.006kg and 0.24 ± 0.002m) respectively with the lowest coefficient of variation (15.8%) in terms of weight were found in Iwoama. The values were significantly different ($P<0.05$) from other locations in terms of weight and total length. Principal component analysis showed that samples from Brass and Iwoama (Bayelsa) formed a separate cluster from samples of other locations. While Ishaka forms an out-group (Figure 2). The correlation matrix showed highly significant correlations between most of the variables (Table 1). However, pre-anal length (PAL) and standard length (SL) were the most correlated ($r= 0.96$; $p<0.01$) while eye diameter (ED) and PAL were the least correlated ($r=0.58$; $p<0.05$). Cluster analysis illustrated by the dendrogram in figure 3 also revealed two major clusters.

3.2   Meristic Analysis

Two components explained 58.05% of the variability (PC-I= 36.59%, PC-II= 21.46%). Dorsal fin count (DFC) shows the highest mean (27.2 ± 0.011) with 3.03% coefficient of variation. In New Calabar, dorsal fin count (DFC) is the parameter with the highest mean value (27 ± 0.01; Coeff. of variation= 3.03%) when compared to other parameters in the location ($P<0.05$). The pair-wise correlation matrix showed highly significant in correlations between most of the variables (Table 2). However, dorsal fin count (DFC) and anal fin count (AFC) (0.371) were the most correlated ($r= 0.37$; $p<0.05$) while pelvic fin count (PVFC) and DFC were the least correlated ($r=0.02$; $p<0.05$). Dendrogram analysis based on meristic data indicated three clusters: Cluster I contain two Sub-groups which includes Epe, Badagry Lagoon, Ishaka and Igbokoda in sub-group A while Oropo Ilape, Brass, Iwoama and river Ethiope in Sub-group B. Cluster II and Cluster III contained New Calabar and Buguma respectively (Figure 6).

Table 1: Correlation matrix between Different Morphometric Characters of *T. guineensis.*

	WT	TL	SL	PDL	PAL	PPL	PPEL	DFL	CFL	AFL	HL	IOW	ED
WT	1.00												
TL	.930[**]	1.00											
SL	.918[**]	.983[**]	1.00										
PDL	.885[**]	.928[**]	.925[**]	1.00									
PAL	.913[**]	.946[**]	.957[**]	.854[**]	1.00								
PPL	.847[**]	.914[**]	.910[**]	.927[**]	.855[**]	1.00							
PPEL	.918[**]	.956[**]	.956[**]	.910[**]	.933[**]	.921[**]	1.00						
DFL	.947[**]	.935[**]	.927[**]	.851[**]	.931[**]	.828[**]	.925[**]	1.00					
CFL	.857[**]	.872[**]	.847[**]	.883[**]	.793[**]	.842[**]	.842[**]	.840[**]	1.00				
AFL	.934[**]	.908[**]	.883[**]	.862[**]	.870[**]	.828[**]	.906[**]	.956[**]	.871[**]	1.00			
HL	.916[**]	.936[**]	.927[**]	.864[**]	.915[**]	.839[**]	.928[**]	.946[**]	.833[**]	.911[**]	1.00		
IOW	.743[**]	.776[**]	.753[**]	.781[**]	.699[**]	.776[**]	.777[**]	.774[**]	.794[**]	.791[**]	.760[**]	1.00	
ED	.616[**]	.660[**]	.632[**]	.620[**]	.576[**]	.624[**]	.662[**]	.631[**]	.635[**]	.604[**]	.685[**]	.654[**]	1.00

**. Correlation is significant at the 0.01 level (2-tailed).

Key: Weight (WT), total length (TL), standard length (SL), Pre-dorsal length (PDL), Pre- anal length (PAL), Pre-pelvic length (PPL), Pre-pectoral length (PPEL), dorsal fin length (DFL), caudal fin length (CFL), anal fin length (AFL), head length (HL), interorbital width (IOW) and Eye diameter (ED).
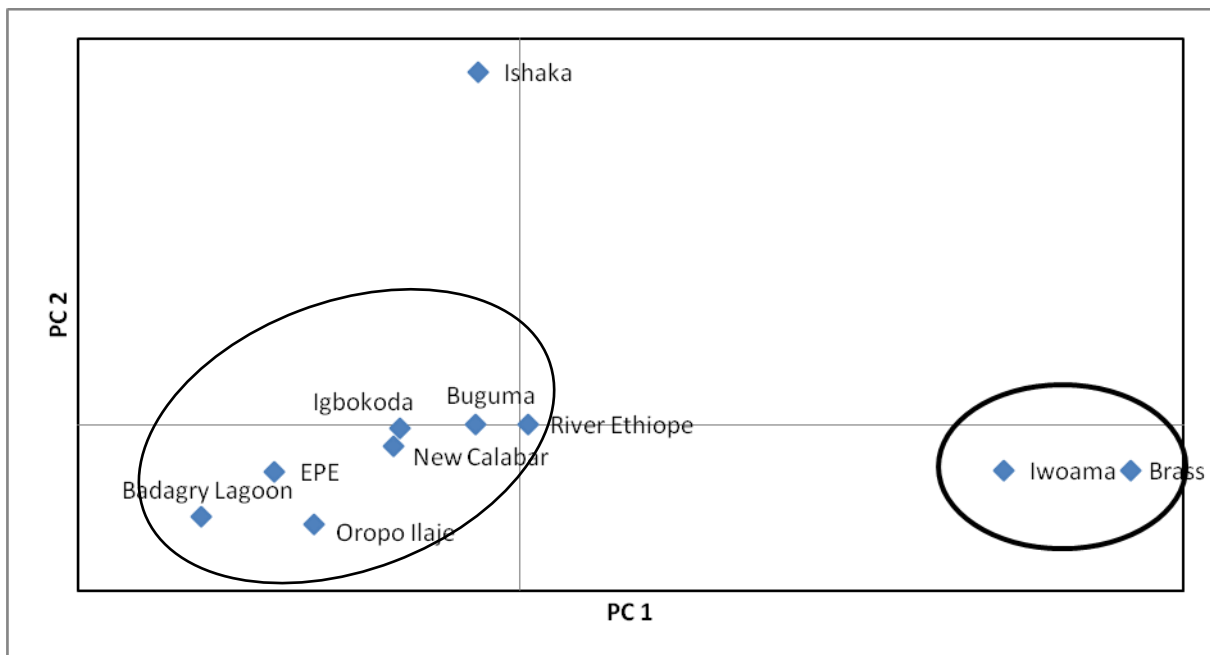

Figure 3: Principal Component Analysis of Morphometric Data Based on Location Distribution of Samples
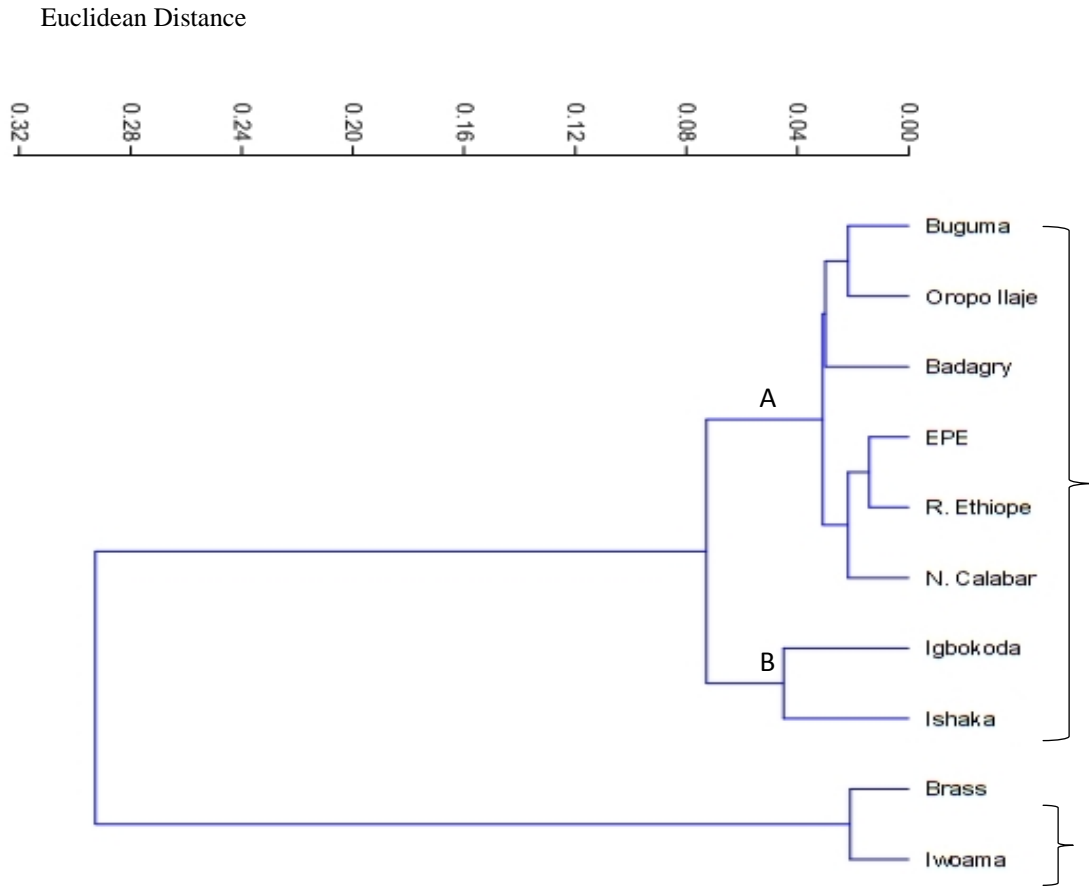
Euclidean Distance

Figure 4: UPGMA Cluster Analysis of Morphometric Bata as Grouped by Location.

Table 2: Correlation Matrix between Different Meristic Characters of *T. guineensis.*

	DFC	AFC	PFC	PVFC	CFC
DFC	1.00				
AFC	.371[**]	1.00			
PFC	.246[**]	.210[**]	1.00		
PVFC	.019	.185[**]	.157[**]	1.00	
CFC	.324[**]	.073	.344[**]	.006	1.00

[**]. Correlation is significant at the 0.01 level (2-tailed).

Key: DFC- dorsal fin count, AFC- anal fin count, PFC- pectoria fin count, PVFC- pelvic fin count and CFC- caudal fin count.
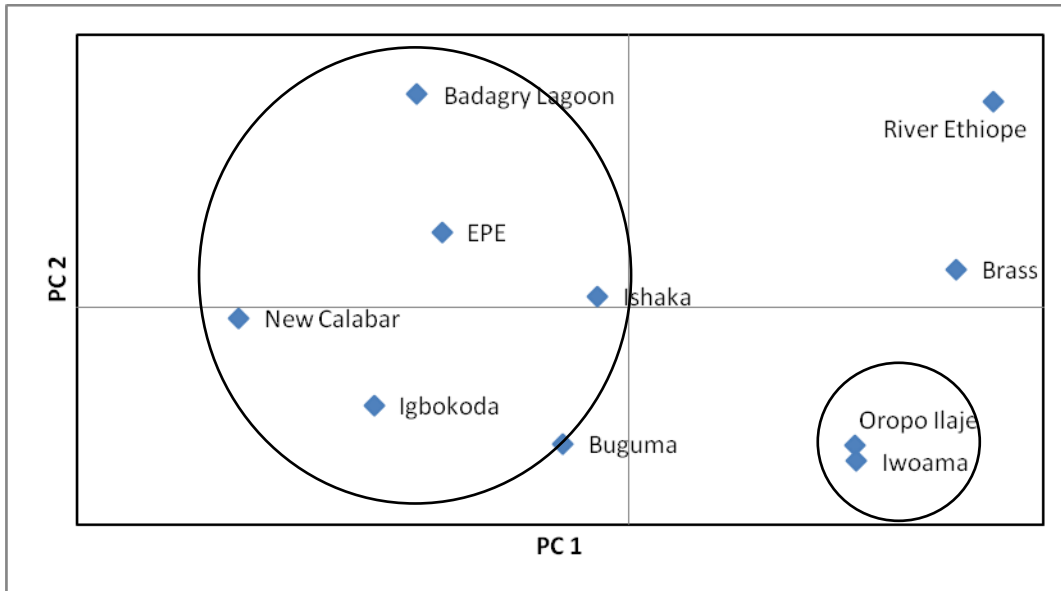
Figure 5: Principal Component Analysis of Meristic Data Based on Location Distribution
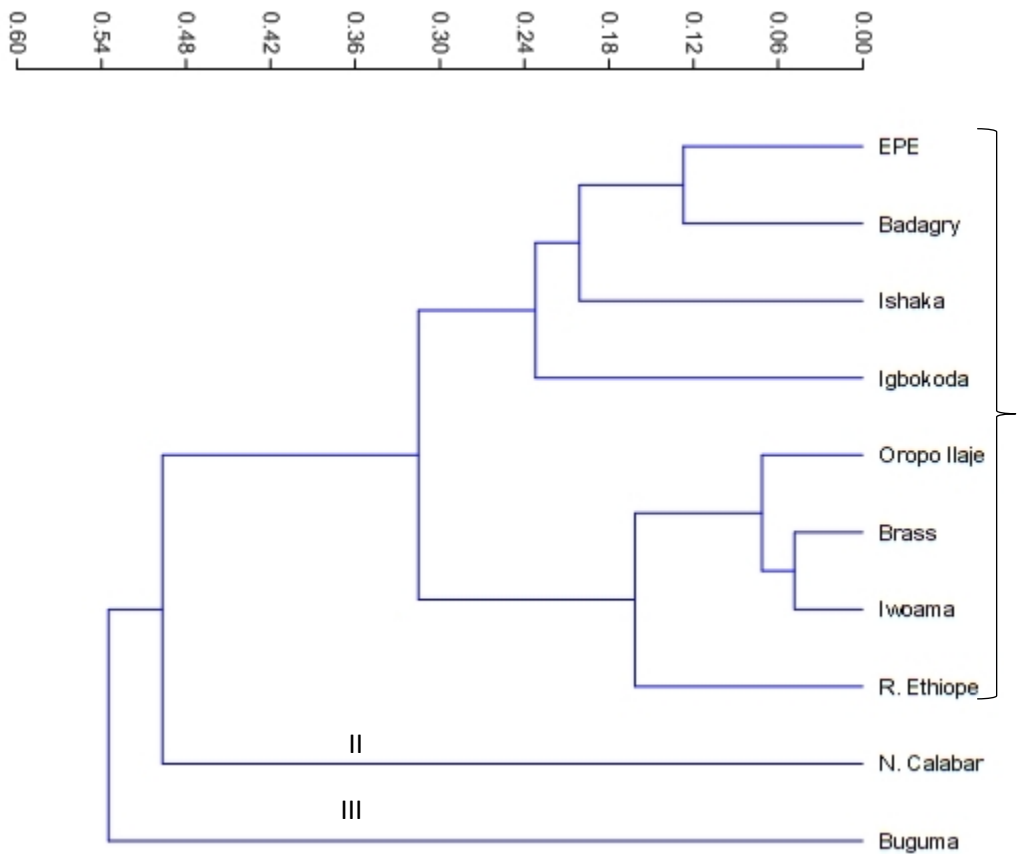
Euclidean Distance

Figure 6: UPGMA Cluster Analysis of Meristic Data Showing Distance Relationship by Location.

Table 3: Correlation Matrix between Different Truss network Characters of *T. guineensis.*

Variables	1-2	1-4	1-3	2-4	4-6	3-4	12-13	3-6	4-5	5-6	5-7	5-8	7-8	7-11	6-8	11-12	11-13
1-2	1.00																
1-4	.855**	1.00															
1-3	.567**	.766**	1.00														
2-4	.833**	.917**	.772**	1.00													
4-6	.831**	.864**	.618**	.799**	1.00												
3-4	-.034	.340**	.503**	.378**	.276**	1.00											
12-13	.771**	.848**	.661	.819**	.920**	.408**	1.00										
3-6	.586**	.795**	.669**	.769**	.845**	.663**	.900**	1.00									
4-5	.560**	.814**	.746**	.843**	.692**	.678**	.783**	.862**	1.00								
5-6	.831**	.929**	.724**	.921**	.895**	.451**	.914**	.886**	.887**	1.00							
5-7	.951**	.904**	.645**	.876**	.897**	.139**	.868**	.731**	.690**	.914**	1.00						
5-8	.350**	.274**	-.006	.282**	.466**	.127*	.439**	.219**	.231**	.421**	.525**	1.00					
7-8	.661**	.393**	.003	.382**	.162**	.511**	.117*	.342**	.138*	.142*	.513**	.174**	1.00				
7-11	.612**	.615**	.467**	.609**	.556**	.124**	.491**	.440**	.472**	.603**	.609**	.029	.419**	1.00			
6-8	.123**	.392**	.409**	.419**	.380**	.649**	.427**	.604**	.608**	.475**	.236**	.027	-.051	.543**	1.00		
11-12	.804**	.921**	.693**	.869**	.810**	.268**	.834**	.751**	.780**	.886**	.856**	.379**	.436**	.558**	.347**	1.00	
11-13	.161**	.282**	.287**	.275**	.164**	.255**	.303**	.256**	.401**	.285**	.215**	.091	-.023	-.038	.096*	.300**	1

**. Correlation is significant at the 0.01 level (2-tailed).

Key: 13 landmarks refer to (1) anterior tip of snout at upper jaw, (2) most posterior aspect of nuerocranium, (3) posterior most point of maxillary, (4) insertion of dorsal fin, (5) origin of dorsal fin, (6) insertion of pelvic fin, (7) insertion of dorsal fin, (8) origin of anal fin, (11) insertion of anal fin, (12) anterior attachment of dorsal membrane, (13) anterior attachment of ventral membrane from caudal fin and (14) posterior end of vertebrae column.
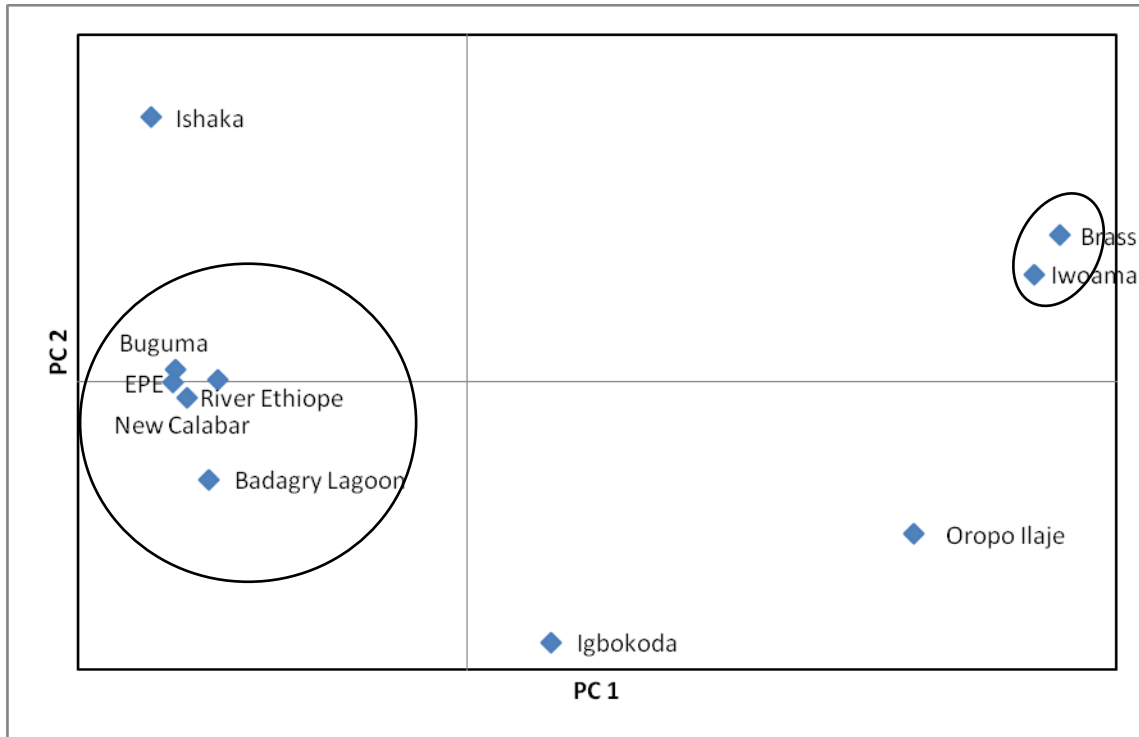
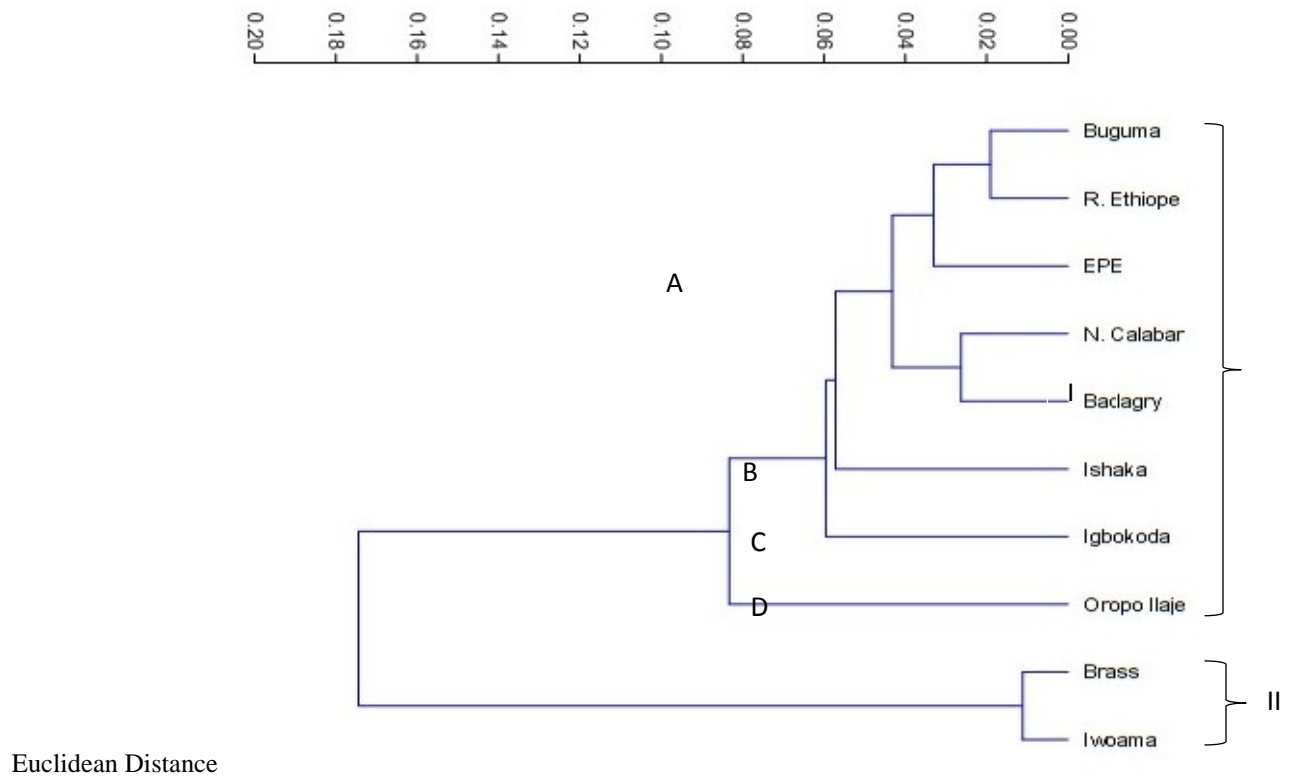**Figure 7:** Principal Component Analysis of Truss network on Location Distribution

Euclidean Distance

Figure 8: UPGMA Cluster Analysis of Truss network as Grouped by Location.

3.3 Truss network system

The first two principal components explained 58.80% of the variability (PC-I= 35.99%, PC-II= 22.81%) with their Eigen values of 6.117 and 3.876 was used to explain the variations. The highest mean length (0.149$\pm$0.001m) with 6.34% coefficient of variation was recorded in Brass location (P<0.05). The pair-wise correlation matrix indicated that among these seventeen variables, from the anterior tip of tilapia at upper jaw (1) to insertion of dorsal fin (4) (1-4) and the origin of dorsal fin (5) to insertion of pelvic fin (6) (5-6) (r=0.929; p<0.05) were the most correlated (Table 3). Dendrogram result of the truss network data showed two clusters: Cluster I consists of Buguma, River Eithiope, Epe, New Calabar and Badary, Ishaka, Igbokoda and Oropo Ilaje while cluster II consists of Brass and Iwoama samples (Figure 7).

4. Discussion

Morphological characters including morphometric, meristic and truss network system have been widely used to delimit the various populations of *Tilapia guineensis* from Nigerian and other coastal waters. Morphometric analysis showed that the ten populations clustered into two distinct groups indicating low variability among the populations of *T. guineensis* from the coastal locations studied. This is in agreement with the report of [9] who pointed out that populations of east coast of Indian Ocean and Pacific Ocean of *P. monodon* are morphologically similar. A similar observation was made by [10] in a Morphometric study of three Populations of Indian Salmon. This relatedness could be attributed to gene flow that might have existed among the populations. Furthermore, the result of the physico-chemical analysis of these locations showed that there were no significant differences among the sampling locations: Thus, must have contributed to relatively low morphological variability observed in the studied populations. This indicates that the observed low variation among the populations probably reflects genetic rather than environmental factors. Since [11] stated that the morphology of a fish or any living being is determined by the interaction between genetic and environmental factors.

The meristic results revealed three clusters instead of two when compared to the morphometric data analysis. This indicates that meristics revealed more variabilityis than morphometrics among the studied populations of *T. guineensis.* This result is consistent with the report of [12] who similarly observed three morphological stocks in *Pomatomus saltatrix* morphological study of the Black sea. Morphological variability among different geographical populations may be attributed due to distinct genetic structure and environmental conditions. Therefore, animals with the same morphometric characters are often assumed to constitute a stock, and this fact has been used widely in stock differentiation in fisheries industry [13]. The PCA plot and dendrogram result of the truss network analysis indicated two major clusters as was observed in morphometric results implying low variability among the studied populations.

We based assessment of genetic variability in *Tilapia guineensis* on morphometric features alone. However, physical features such as morphometric attributes are sometimes adaptive reflecting convergent evolution. Thus, it is often necessary to complement morphometric analysis with molecular data. Future work in our laboratory will be focused on assessment of genetic variability in *Tilapia guineensis* using microsatellite markers.

5. Conclusion

In the current study, meristics revealed more variability than morphometrics and truss network system in differentiating the morphological stocks of *Tilapia guineensis.* This could be due to the fact that meristic variables have stronger genetic basis since they are fixed early during development and are therefore not influenced significantly by environmental factors [14].

6. Recommendation

Meristic method is more effective and should be recommended for *Tilapia guineensis* differentiation, possibly in conjunction with other morphological and molecular analysis.

Acknowledgement

References

[1] Trewavas E. Tilapiine fishes of the genera Sarotherodon, Oreochromis and Danakilia.british museum, *Natural History*, London. 1993.

[2] Nelson JS. Fishes of the World: John wiley and sons, inc. pp.3-5. 2006.

[3] Hockaday S., Beddow, T.A., Stone, M., Hancock, P. and Ross, L.G. Using truss networks to estimate the biomass of Oreochromis niloticus and to investigate shape characters. *Journal of Fish Biology*, **57**: 981-1000. 2000.

[4] Corti, M., Thorpe, R. S., Sola, L., Sbordoni, V. and Cataudella, S., Multivariate morphometrics in aquaculture: a case study of six stocks of the common carp (Cyprinus carpio) from Italy. *Canadian Journal of Fish Aquatic Science* **45**: 1548-1554. 1998

[5] Murta, A.G. Morphological variation of horse mackerel (*Trachurus trachurus*) in the Iberian and North African Atlantic: implications for stock identification. ICES *Journal of Marine Science* **57**: 1240-1248. 2000.

[6] Allendorf, F; Ryman N; and Utter F. Genetics and Fishery Management: Past, Present, and Future. In: N. Ryman (ed.). Population Genetics and Fishery Management. *The University of Washington*, USA. p 1-20. 1987.

[7] Sathianandan, T.V.. Truss network analysis for fish genetic stock discrimination, In: Winter School on Recent Advances in Mariculture Genetics and Biotechnology. pp.1-10. 2003.

[8] Statistical Tool for Research (STAR) V.2.0.1 Biometrics and Breeding informatics, PBGB Division , International Rice Research Institute , Los Banos, Lagum. 2014.

[9] Sun, M.M., Huang, J. H., Jiang, S. G., Yang, Q. B., Zhou, F. L., Zhu, C. Y., Yang, L. S., Su, T. F.,. Morphometric analysis of four different populations of Penaeus monodon (Crustacea, Decapoda, Penaeidae). *Aquaculture. Research*, **45**: 113–123. 2012.

[10] Thirumaraiselvi, R., Thangaraj*, M., Ramanadevi,V. Morphometric and Genetic Variation in Three

Populations of Indian Salmon (*Polydactylus plebeius*).Not *Science Biology* **5**(3): 275-281. 2013.

[11] Swain, D.P. and Foote, C.J. Stocks and chameleons the use of phenotypic variation in stock identification. *Fish Research* **43**: 113-128. 1999.

[12] Turan C, Oral M, Ozturk B, Duzgunes E. Morphometric and meristic variation between stocks of Bluefish (*Pomatomus saltatrix*) in the Black, Marmara, Aegean and northeastern Mediterranean Seas. *Fish Research* **79**:139-147. 2006.

[13] Dwivedi, A. K., Dubey, V. K.,. Advancements in morphometric differentiation: A review on stock identification among fish populations. *Revised Fisheries Biology Fisher*, **23**: 23-39. 2013.

[14] Samaradivakara, S.P, N.Y. Hirimuthugoda1* R.H.A.N.M. Gunawardana1, R.J. Illeperuma2 N.D. Fernandopulle2, A.D. De Silva2 and P.A.B.D. Alexander3. Morphological Variation of Four Tilapia Populations in Selected Reservoirs in Sri Lanka. *Journal of Tropical Agricultural Research*. **23** (2): 105 – 116. 2012.